



PCT09

ENTERED

RAW SEQUENCE LISTING

DATE: 12/13/2002 P.6

PATENT APPLICATION: US/09/763,994A

TIME: 10:19:00

Input Set : A:\EP.txt

Output Set: N:\CRF4\12132002\I763994A.raw

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3 <110> APPLICANT: Edmonds, Brian T.
5 <120> TITLE OF INVENTION: HUMAN LATENT TRANSFORMING GROWTH FACTOR-BETA BINDING
6 PROTEIN 3
7 <130> FILE REFERENCE: X-12239
10 <140> CURRENT APPLICATION NUMBER: US/99/763,994A
C--> 11 <141> CURRENT FILING DATE: 2001-10-15
13 <160> NUMBER OF SEQ ID NOS: 6
15 <170> SOFTWARE: PatentIn Ver. 2.0
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 3624
19 <212> TYPE: DNA
20 <213> ORGANISM: Homo sapiens
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26 gggggggggg gggggggggg gggggggggg gggggggggg gggggggggg gggggggggg 240
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54 ctgtgggggg acggggggtt ctgcatcaac ttcccggtc actacaagtg caactggtac 1920
55 cccgggtacc ggcctaaaagc ctcccggtct cctggtgtgg aagacataga cgagtgcgg 1980
56 gacccaagct ctggcccgga tggcaaatgc gagaacaagg cggggagctt caagtgcata 2040
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58 ggcgaggcca ggcctgtctc ggcctggctg tggcagaacc tccggggctc ctcccggtgc 2160
59 acctgtgccc aggtctatga gcacgggccc gagggtccga gttggttggg tctggcagag 2220
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81 gcagagtgcc gagagctgaa ccagcgcggg ctgctgtgca agagcgagcg ctggtgaa 3540
82 accaggggtt cctcccgctg cgtctgcaaa gccggcttc cgcgcagcgc ccgcacgggg 3600
83 ggcgtgcctc ccagcgctcg cggc 3624

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#3 <210> SEQ ID NO: 2

#4 <211> LENGTH: 1203

#5 <212> TYPE: PRK

#6 <213> ORGANISM: Homo sapiens

#7 <400> SEQUENCE: 2

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92      1          5          10          15
93 Val Phe Ala Pro Val Ile Cys Lys Arg Thr Cys Leu Lys Gly Gln Cys
94      20          25          30
95 Arg Asp Ser Cys Gln Glu Gly Ser Asn Met Thr Leu Ile Gly Glu Asn
96      35          40          45
97 Gly His Ser Thr Asp Thr Leu Thr Gly Ser Gly Phe Arg Val Val Val
98      50          55          60
99 Cys Pro Leu Pro Cys Met Asn Gly Gly Gln Cys Ser Ser Arg Asn Gln
100     65          70          75          80
101 Cys Leu Cys Pro Pro Asp Phe Thr Gly Arg Phe Cys Gln Val Pro Ala
102     85          90          95
103 Gly Gly Ala Gly Gly Gly Thr Gly Gly Ser Gly Pro Gly Leu Ser Arg

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110          100          105          110
111 Thr Gly Ala Leu Ser Thr Gly Ala Leu Pro Pro Leu Ala Pro Glu Gly
112          115          120          125
113 Asp Ser Val Ala Ser Lys His Ala Ile Tyr Ala Val Gln Val Ile Ala
114          130          135          140
115 Asp Pro Pro Gly Pro Gly Glu Gly Pro Pro Ala Gln His Ala Ala Phe
116          145          150          155          160
117 Leu Val Pro Leu Gly Pro Gly Gln Ile Ser Ala Glu Val Gln Ala Pro
118          165          170          175
119 Pro Pro Val Val Asn Val Arg Val His His Pro Pro Glu Ala Ser Val
120          180          185          190
121 Gln Val His Arg Ile Glu Ser Ser Asn Ala Gln Ser Ala Ala Pro Ser
122          195          200          205
123 Gln His Leu Leu Pro His Pro Lys Pro Ser His Pro Arg Pro Pro Thr
124          210          215          220
125 Gln Lys Ser Leu Gly Arg Cys Phe Gln Asp Thr Leu Pro Lys Gln Pro
126          225          230          235          240
127 Cys Gly Ser Asn Pro Leu Pro Gly Leu Thr Lys Gln Glu Asp Cys Cys
128          245          250          255
129 Gly Ser Ile Gly Thr Ala Trp Gly Gln Ser Lys Cys His Lys Cys Pro
130          260          265          270
131 Gln Leu Gln Tyr Thr Gly Val Gln Lys Pro Gly Pro Val Arg Gly Glu
132          275          280          285
133 Val Gly Ala Asp Cys Pro Gln Gly Tyr Lys Arg Leu Asn Ser Thr His
134          290          295          300
135 Cys Gln Asp Ile Asn Gln Cys Ala Met Pro Gly Val Cys Arg His Gly
136          305          310          315
137 Asp Cys Leu Asn Asn Pro Gly Ser Tyr Arg Cys Val Cys Pro Pro Gly
138          320          325          330
139 His Ser Leu Gly Pro Ser Arg Thr Gln Cys Ile Ala Asp Lys Pro Glu
140          335          340          345          350
141 Glu Lys Ser Leu Cys Phe Arg Leu Val Ser Pro Glu His Gln Cys Gln
142          355          360          365
143 His Pro Leu Thr Thr Arg Leu Thr Arg Gln Leu Cys Cys Cys Ser Val
144          370          375          380
145 Gly Lys Ala Trp Gly Ala Arg Cys Gln Arg Cys Pro Thr Asp Gly Thr
146          385          390          395          400
147 Ala Ala Phe Lys Glu Ile Cys Pro Ala Gly Lys Gly Tyr His Ile Leu
148          405          410          415
149 Thr Ser His Gln Thr Leu Thr Ile Gln Gly Glu Ser Asp Phe Ser Leu
150          420          425          430
151 Phe Leu His Pro Asp Gly Pro Pro Lys Pro Gln Gln Leu Pro Glu Ser
152          435          440          445
153 Pro Ser Gln Ala Pro Pro Pro Glu Asp Thr Glu Glu Glu Arg Gly Val
154          450          455          460
155 Thr Thr Asp Ser Pro Val Ser Glu Glu Arg Ser Val Gln Gln Ser His
156          465          470          475          480
157 Pro Thr Ala Thr Thr Pro Ala Arg Pro Tyr Pro Glu Leu Ile Ser
158          485          490          495

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184 Arg Pro Ser Pro Pro Thr Met Arg Trp Phe Leu Pro Asp Leu Pro Pro
185          500          505          510
187 Ser Arg Ser Ala Val Glu Ile Ala Pro Thr Gln Val Thr Glu Thr Asp
188          515          520          525
190 Glu Cys Arg Leu Asn Gln Asn Ile Cys Gly His Gly Glu Cys Val Pro
191          530          535          540
193 Gly Pro Pro Asp Tyr Ser Cys His Cys Asn Pro Gly Tyr Arg Ser His
194 545          550          555          560
196 Pro Gln His Arg Tyr Cys Val Asp Val Asn Glu Cys Glu Ala Glu Pro
197          565          570          575
199 Cys Gly Pro Gly Arg Gly Ile Cys Met Asn Thr Gly Gly Ser Tyr Asn
200          580          585          590
202 Cys His Cys Asn Arg Gly Tyr Arg Leu His Val Gly Ala Gly Gly Arg
203          595          600          605
205 Ser Cys Val Asp Leu Asn Glu Cys Ala Lys Pro His Leu Cys Gly Asp
206          610          615          620
208 Gly Gly Phe Cys Ile Asn Phe Pro Gly His Tyr Lys Cys Asn Cys Tyr
209 625          630          635          640
211 Pro Gly Tyr Arg Leu Lys Ala Ser Arg Pro Pro Val Cys Gln Asp Ile
212          645          650          655
214 Asp Gln Cys Arg Asp Pro Ser Ser Cys Pro Asp Gly Lys Cys Gln Asn
215          660          665          670
217 Lys Pro Gly Ser Phe Lys Cys Ile Ala Cys Gln Pro Gly Tyr Arg Ser
218          675          680          685
220 Gln Gly Gly Gly Ala Cys Arg Asp Val Asn Glu Cys Ala Glu Gly Ser
221          690          695          700
223 Pro Cys Ser Pro Gly Trp Cys Gln Asn Leu Pro Gly Ser Phe Arg Cys
224 705          710          715          720
226 Thr Cys Ala Gln Gly Tyr Ala Pro Ala Pro Asp Gly Arg Ser Cys Leu
227          725          730          735
229 Asp Val Asp Gln Cys Gln Ala Gly Asp Val Cys Asp Asn Gly Ile Cys
230          740          745          750
232 Ser Asn Thr Pro Gly Ser Phe Gln Cys Gln Cys Leu Ser Gly Tyr His
233          755          760          765
235 Leu Ser Arg Asp Arg Ser His Cys Glu Asp Ile Asp Glu Cys Asp Phe
236          770          775          780
238 Pro Ala Ala Cys Ile Gly Gly Asp Cys Ile Asn Thr Asn Gly Ser Tyr
239 785          790          795          800
241 Arg Cys Leu Cys Pro Gln Gly His Arg Leu Val Gly Gly Arg Lys Cys
242          805          810          815
244 Gln Asp Ile Asp Glu Cys Ser Gln Asp Pro Ser Leu Cys Leu Pro His
245          820          825          830
247 Gly Ala Cys Lys Asn Leu Gln Gly Ser Tyr Val Cys Val Cys Asp Glu
248          835          840          845
250 Gly Phe Thr Pro Thr Gln Asp Gln His Gly Tyr Gln Glu Val Gln Gln
251          850          855          860
253 Pro His His Lys Lys Glu Cys Tyr Leu Asn Phe Asp Asp Thr Val Phe
254 865          870          875          880
256 Cys Asp Ser Val Leu Ala Thr Asn Val Thr Gln Gln Glu Cys Cys Cys

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257          885          890          895
259 Ser Leu Gly Ala Gly Trp Gly Asp His Cys Glu Ile Tyr Pro Cys Pro
260          900          905          910
262 Val Tyr Ser Ser Ala Glu Phe His Ser Leu Cys Pro Asp Gly Lys Gly
263          915          920          925
265 Tyr Thr Gln Asp Asn Asn Ile Val Asn Tyr Gly Ile Pro Ala His Arg
266          930          935          940
268 Asp Ile Asp Glu Cys Met Leu Phe Gly Ser Glu Ile Cys Lys Glu Gly
269 945          950          955          960
271 Lys Cys Val Asn Thr Gln Pro Gly Tyr Glu Cys Tyr Cys Lys Gln Gly
272          965          970          975
274 Phe Tyr Tyr Asp Gly Asn Leu Leu Glu Cys Val Asp Val Asp Glu Cys
275          980          985          990
277 Leu Asp Glu Ser Asn Cys Arg Asn Gly Val Cys Glu Asn Thr Arg Gly
278          995          1000          1005
280 Gly Tyr Arg Cys Ala Cys Thr Pro Pro Ala Glu Tyr Ser Pro Ala Gln
281          1010          1015          1020
283 Arg Gln Cys Leu Ser Pro Glu Glu Met Glu Arg Ala Pro Glu Arg Arg
284 1025          1030          1035          1040
286 Asp Val Cys Trp Ser Gln Arg Gly Glu Asp Gly Met Cys Ala Gly Pro
287          1045          1050          1055
289 Leu Ala Gly Pro Ala Leu Thr Phe Asp Asp Cys Cys Cys Arg Gln Gly
290          1060          1065          1070
292 Arg Gly Trp Gly Ala Gln Cys Arg Pro Cys Pro Pro Arg Gly Ala Gly
293          1075          1080          1085
295 Ser His Cys Pro Thr Ser Gln Ser Glu Ser Asn Ser Phe Trp Asp Thr
296          1090          1095          1100
298 Ser Pro Leu Leu Leu Gly Lys Pro Pro Arg Asp Glu Asp Ser Ser Glu
299 1105          1110          1115          1120
301 Glu Asp Ser Asp Glu Cys Arg Cys Val Ser Gly Arg Cys Val Pro Arg
302          1125          1130          1135
304 Pro Gly Gly Ala Val Cys Glu Cys Pro Gly Gly Phe Gln Leu Asp Ala
305          1140          1145          1150
307 Ser Arg Ala Arg Cys Val Asp Ile Asp Glu Cys Arg Glu Leu Asn Gln
308          1155          1160          1165
310 Arg Gly Leu Leu Cys Lys Ser Glu Arg Cys Val Asn Thr Ser Gly Ser
311          1170          1175          1180
313 Phe Arg Cys Val Cys Lys Ala Gly Phe Ala Arg Ser Arg Pro His Gly
314 1185          1190          1195          1200
316 Ala Cys Val Pro Gln Arg Arg Arg
317          1205
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321 <111> LENGTH: 3771
322 <112> TYPE: DNA
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324 <400> SEQUENCE: 3
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326 gtgatctgca agcggacgtg tctcaagggc cagtctgggg acagttgtca gaagggtccc 120
327 aacatgacgc tcctcggaga gaacggccac agcacagaca cgttcacggg ctccggcttc 180

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/763,994A

DATE: 12/13/2002
TIME: 10:19:04

Input Set : A:\EP.txt
Output Set: N:\CRF4\12132002\I763994A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:6; Xaa Pos. 189

VARIABLE LOCATION SUMMARY

DATE: 12/13/2002

PATENT APPLICATION: US/09/763,994A

TIME: 10:19:04

Input Set : A:\EP.txt

Output Set : N:\CRF4\12132002\I763994A.raw

Use of n's or Xaa's (NEW RULES) :

Use of n's and/or Xaa's have been detected in the Sequence Listing.

Use of <220> to <223> is MANDATORY if n's or Xaa's are present.

in <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

Seq#:6; Xaa Pos. 189

VERIFICATION SUMMARY

DATE: 12/13/2002

PATENT APPLICATION: US/09/763,994A

TIME: 10:19:04

Input Set : A:\EP.txt

Output Set: N:\CRF4\12132002\I763994A.raw

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:495 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:6
L:495 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:6
L:495 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:176